

**WEST**

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L1: Entry 2 of 30

File: USPT

Dec 8, 1998

US-PAT-NO: 5846751

DOCUMENT-IDENTIFIER: US 5846751 A

TITLE: Test kits and methods for detecting H. pylori

DATE-ISSUED: December 8, 1998

INT-CL: [6] G01N 33/554, G01N 33/53

US-CL-ISSUED: 435/7.32; 435/7.2, 435/7.92, 435/7.93

US-CL-CURRENT: 435/7.32; 435/7.2, 435/7.92, 435/7.93

FIELD-OF-SEARCH: 435/7.92, 435/79.3, 435/7.32, 435/7.94, 435/7.5

.2

530/350

424/234.1

424/+

536

Anti Hp antibody may vary with strain used as antigen possibly due to serological diversity.

MIZUTA TOSHIMI (1); INOUE HIROYUKI (1); HAYASHI TOMOKO (1); SHIMOYAMA TAKASHI (1)

(1) Hyogo College of Medicine

Nippon Rinsho(Japanese Journal of Clinical Medicine), 1993 , VOL.51,NO.12 , PAGE.3087-3093, FIG.7, TBL.2, REF.14

JOURNAL NUMBER: Z0679AAD ISSN NO: 0047-1852

UNIVERSAL DECIMAL CLASSIFICATION: 616.9

LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan

DOCUMENT TYPE: Journal

ARTICLE TYPE: Commentary

MEDIA TYPE: Printed Publication

DESCRIPTORS: human(primates); **Helicobacter** ; clinical isolate; bacterial infection(disease); bacterial antigen; monoclonal antibody; serotype; **Helicobacter pylori**

BROADER DESCRIPTORS: spiral and curved bacteria; bacterium; microorganism; infectious disease; disease; antigen; antibody

CLASSIFICATION CODE(S): GD01010H

2/9/2 (Item 2 from file: 94)

DIALOG(R)File 94:JICST-EPlus

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01795429 JICST ACCESSION NUMBER: 93A0616221 FILE SEGMENT: JICST-E

**Evaluation of a Rapid Urease Test and the Helico-G ELISA for Diagnosis Helicobacter pylori Infection.**

FUKUDA YOSHIHIRO (1); YAMAMOTO ISSEI (1); TAKAMI SHIGETO (1); TONOKATSU YASUSHI (1); MIZUTA TOSHIMI (1); TSUYUGUCHI TAKAICHI (1); INOUE HIROYUKI (1); TAMURA KAZUTAMI (1); SHIMOYAMA TAKASHI (1)

(1) Hyogo College of Medicine

Kiso to Rinsho(Clinical Report), 1993 , VOL.27,NO.8, PAGE.3336-3347, FIG.2, TBL.8, REF.23

JOURNAL NUMBER: Z0357AAI ISSN NO: 0385-2806

UNIVERSAL DECIMAL CLASSIFICATION: 615.2.03:616-07 616.9-07 616.3-085

LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan

DOCUMENT TYPE: Journal

ARTICLE TYPE: Original paper

MEDIA TYPE: Printed Publication

ABSTRACT: A rapid urease test and the Helico-G ELISA for the detection of **Helicobacter pylori** infection were evaluated using gastric biopsy specimens and serum from 102 patients attending our endoscopy clinic. The efficacy of them were assessed in relation to the detection by culture of H. pylori on gastric mucosal biopsy specimens. The rapid urease test was 90.5% sensitive and 80.0% specific and the Helico-G ELISA was 91.2% sensitive and 69.0% specific for H. pylori infection. These results suggest that the rapid urease test and Helico-G ELISA are useful for diagnosis of H. pylori infection and available to routine diagnosis in clinics. (author abst.)

DESCRIPTORS: human(primates); clinical laboratory test; digestive system disease; **Helicobacter** ; diagnostic drug; bacterial infection(disease); measurement accuracy; urease; ELISA; enzyme activity

BROADER DESCRIPTORS: medical examination; inspection; diagnosis; disease; spiral and curved bacteria; bacterium; microorganism; drug; infectious disease; accuracy; degree; amide hydrolase; hydrolase; enzyme; enzyme antibody technique; labeled antibody method; immunoassay; bioassay

CLASSIFICATION CODE(S): GW20020A; GD01020S; GH05020G

?logoff hold

--CY; Hybridomas--drug effects--DE; Mice; Polyribosomes--drug effects--DE;  
Polyribosomes--metabolism--ME; Serum Albumin, Bovine--pharmacology--PD;  
Translation, Genetic--drug effects--DE

CAS Registry No.: 0 (Antibodies, Monoclonal); 0 (Culture Media); 0  
(Proteins); 0 (Serum Albumin, Bovine)  
Record Date Created: 19890825  
Record Date Completed: 19890825

15/9/21 (Item 5 from file: 5)  
DIALOG(R) File 5: Biosis Previews(R)  
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0009262120 BIOSIS NO.: 199497283405

**Three tuf-like genes in the kirromycin producer *Streptomyces ramocissimus***  
AUTHOR: Vijgenboom E (Reprint); Woudt L P; Heinstra P W H; Rietveld K; Van  
Haarlem J; Van Wezel G P; Shochat S; Bosch L  
AUTHOR ADDRESS: Dep. Biochem., Leiden Univ., Gorlaeus Lab., PO Box 9402,  
2300 RA Leiden, Netherlands\*\*Netherlands  
JOURNAL: Microbiology (Reading) 140 (4): p983-998 1994 1994  
DOCUMENT TYPE: Article  
RECORD TYPE: Abstract  
LANGUAGE: English

ABSTRACT: We have identified, cloned and sequenced three tuf-like genes from *Streptomyces ramocissimus* (Sr.), the producer of the antibiotic kirromycin which inhibits protein synthesis by binding the polypeptide chain elongation factor EF-Tu. The tuf-1 gene encodes a protein with 71% amino acid residues identical to the well characterized elongation factor Tu of *Escherichia coli* (Ec.EF-Tu). The genetic location of tuf-1 downstream of a fus homologue and the in vitro activity of Sr.EF-Tu1 show that tuf-1 encodes a genuine EF-Tu. The putative Sr.EF-Tu2 and Sr.EF-Tu3 proteins are 69% and 63% identical to Ec. EFTu. Homologues of tuf-1 and tuf-3 were detected in all five *Streptomyces* strains investigated, but tuf-2 was found in *S. ramocissimus* only. The three tuf genes were expressed in *E. coli* and used to produce polyclonal antibodies. Western blot analysis showed that Sr.EF-Tu1 was present at all times under kirromycin production conditions in submerged and surface-grown cultures of *S. ramocissimus* and in germinating spores. The expression of tuf-2 and tuf-3 was, however, below the detection level. Surprisingly, Sr.EF-Tu1 was kirromycin sensitive, which excludes the possibility that EF-Tu is involved in the kirromycin resistance of *S. ramocissimus*.

REGISTRY NUMBERS: 50935-71-2: KIRROMYCIN

DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Enzymology--  
Biochemistry and Molecular Biophysics; Genetics; Molecular Genetics--  
Biochemistry and Molecular Biophysics; Pharmacology; Physiology  
BIOSYSTEMATIC NAMES: Enterobacteriaceae--Facultatively Anaerobic  
Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms;  
Streptomyces and Related Genera--Actinomycetes and Related Organisms,  
Eubacteria, Bacteria, Microorganisms  
ORGANISMS: *Escherichia coli* (Enterobacteriaceae); *Streptomyces*  
*ramocissimus* (Streptomyces and Related Genera); Streptomyces  
(Streptomyces and Related Genera)  
COMMON TAXONOMIC TERMS: Bacteria; Eubacteria; Microorganisms  
CHEMICALS & BIOCHEMICALS: KIRROMYCIN  
MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence; molecular sequence  
data; nucleotide sequence; X67057--EMBL; X67058--EMBL; X67059--EMBL  
MISCELLANEOUS TERMS: ANTIBIOTIC RESISTANCE MECHANISM; ELONGATION FACTOR  
TU TUF-1 GENE; HOMOLOGY; TUF-2 GENE; TUF-3 GENE

CONCEPT CODES:

10010 Comparative biochemistry  
10062 Biochemistry studies - Nucleic acids, purines and pyrimidines  
10064 Biochemistry studies - Proteins, peptides and amino acids  
10300 Replication, transcription, translation  
10506 Biophysics - Molecular properties and macromolecules  
10802 Enzymes - General and comparative studies: coenzymes  
10806 Enzymes - Chemical and physical

13012 Metabolism - Proteins, peptides and amino acids  
22002 Pharmacology - General  
31000 Physiology and biochemistry of bacteria  
31500 Genetics of bacteria and viruses  
38504 Chemotherapy - Antibacterial agents  
39004 Food microbiology - Antibiotics, biologics and other agents  
BIOSYSTEMATIC CODES:  
06702 Enterobacteriaceae  
08840 Streptomycetes and Related Genera

15/9/25 (Item 9 from file: 5)  
DIALOG(R) File 5:Biosis Previews(R)  
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0004584652 BIOSIS NO.: 198579003551  
MONOCLONAL ANTIBODY SPECIFIC FOR YEAST ELONGATION FACTOR 3  
AUTHOR: HUTCHISON J S (Reprint); FEINBERG B; ROTHWELL T C; MOLDAVE K  
AUTHOR ADDRESS: DEP BIOL CHEM, COLL MED, UNIV CALIF, IRVINE, IRVINE, CA  
92717, USA\*\*USA  
JOURNAL: Biochemistry 23 (13): p3055-3063 1984  
ISSN: 0006-2960  
DOCUMENT TYPE: Article  
RECORD TYPE: Abstract  
LANGUAGE: ENGLISH

ABSTRACT: Hybridomas were prepared by fusing mouse myeloma (P3 .times. 63 Ag8) cells of mice immunized with a yeast fraction enriched with respect to nonribosomal translational components. Cloned hybridoma lines were grown in the form of ascites tumors, and the **monoclonal antibodies** produced were purified from the ascites fluid by chromatography on DEAE-Affi-Gel Blue. One of the **antibodies**, from a hybridoma cell line designated as PSH-1, inhibited the translation of natural mRNA and poly(U) and polysomal chain elongation in a cell-free protein-synthesizing system from yeast. Resolution and partial purification of the elongation factors [EF] indicated that the **monoclonal antibody** from PSH-1 did not interact with EF-1 or EF-2 but reacted with and inactivated EF-3, the 125,000 MW additional elongation factor specifically required with yeast ribosomes. The EF-3 purified from the cytosol by immunoaffinity chromatography was comparable to that prepared by ion-exchange chromatography. Evidently, EF-3 was essential for the translation of natural mRNA as well as poly(U), was associated with polysomes but not ribosomal subunits, and was required for every cycle in the elongation phase of protein synthesis.

DESCRIPTORS: MOUSE MYELOMA P-3-X-63-AG-8 CELL MOUSE SPLEEN CELL MOUSE HYBRIDOMA PSH-1 CELL ASCITES FLUID RIBOSOME POLYSOMAL CHAIN **ELONGATION** MESSENGER RNA **TRANSLATION** ASCITES TUMOR CLONE  
DESCRIPTORS:

MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Genetics; **Immune** System--Chemical Coordination and Homeostasis; Metabolism; Molecular Genetics--Biochemistry and Molecular Biophysics; Physiology; Tumor Biology  
BIOSYSTEMATIC NAMES: Ascomycetes--Fungi, Plantae; Muridae--Rodentia, Mammalia, Vertebrata, Chordata, Animalia  
COMMON TAXONOMIC TERMS: Fungi; Microorganisms; Nonvascular Plants; Plants ; Animals; Chordates; Mammals; Nonhuman Vertebrates; Nonhuman Mammals; Rodents; Vertebrates

CONCEPT CODES:  
02506 Cytology - Animal  
03506 Genetics - Animal  
10050 Biochemistry methods - General  
10054 Biochemistry methods - Proteins, peptides and amino acids  
10058 Biochemistry methods - Carbohydrates  
10060 Biochemistry studies - General  
10062 Biochemistry studies - Nucleic acids, purines and pyrimidines  
10064 Biochemistry studies - Proteins, peptides and amino acids  
10068 Biochemistry studies - Carbohydrates  
10300 Replication, transcription, translation

10504 Biophysics - Methods and techniques  
 10506 Biophysics - Molecular properties and macromolecules  
 11314 Chordate body regions - Abdomen  
 12100 Movement  
 13014 Metabolism - Nucleic acids, purines and pyrimidines  
 15001 Blood - General and methods  
 15006 Blood - Blood, lymphatic and reticuloendothelial pathologies  
 15008 Blood - Lymphatic tissue and reticuloendothelial system  
 15010 Blood - Other body fluids  
 18200 Coelomic membranes, mesenteries and related structures  
 24003 Neoplasms - Immunology  
 24005 Neoplasms - Neoplastic cell lines  
 24010 Neoplasms - Blood and reticuloendothelial neoplasms  
 34502 Immunology - General and methods  
 34508 Immunology - Immunopathology, tissue immunology  
 51522 Plant physiology - Chemical constituents  
 BIOSYSTEMATIC CODES:  
 15100 Ascomycetes  
 86375 Muridae

15/9/27 (Item 1 from file: 34)  
 DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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05220152 Genuine Article#: VH925 Number of References: 46  
**Title: IDENTIFICATION OF AN EF-TU PROTEIN THAT IS PERIPLASM-ASSOCIATED AND PROCESSED IN NEISSERIA-GONORRHOEAE**  
 Author(s): PORCELLA SF; BELLAND RJ; JUDD RC  
 Corporate Source: UNIV TEXAS, SW MED SCH, DEPT MICROBIOL/DALLAS//TX/75235; NIAID, ROCKY MT LABS, NIH/HAMILTON//MT/59840; UNIV MONTANA, DIV BIOL SCI/MISSOULA//MT/59812  
 Journal: MICROBIOLOGY-UK, 1996, V142, SEP (SEP), P2481-2489  
 ISSN: 1350-0872  
 Language: ENGLISH Document Type: ARTICLE  
 Geographic Location: USA  
 Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences  
 Journal Subject Category: MICROBIOLOGY  
**Abstract:** A 44 kDa protein is a dominant component of periplasmic extracts of *Neisseria gonorrhoeae*. Peptide sequence generated from a cyanogen-bromide-cleaved fragment of this protein indicated sequence homology with elongation factor-Tu (EF-Tu). **Polyclonal antiserum** was made against the 44 kDa protein purified from periplasm extracts of *N. gonorrhoeae*. The preabsorbed **antiserum** was immunoblotted against whole-cell lysates on two-dimensional gels. A 44 kDa protein and a smaller 37 kDa protein were recognized by this **antiserum**. A *N. gonorrhoeae* lambda phage DNA library was screened and a clone expressing a 44 kDa protein was identified. The DNA insert in this clone contained several genes homologous to genes contained in the str operon of *Escherichia coli*. One ORF product with a calculated molecular mass of 43 kDa was highly homologous to the EF-TuA of *E. coli*. A synthetic peptide **antiserum** specific for a portion of the C terminus of EF-Tu confirmed that the 37 kDa protein in whole-cell lysates of *N. gonorrhoeae* was a processed form of EF-Tu. Deletion of the tufA gene homologue in *N. gonorrhoeae* was attempted but was unsuccessful.  
**Descriptors--Author Keywords:** NEISSERIA GONORRHOEAE ; TUFA ; **EF-TU** ; PROCESSING  
**Identifiers--KeyWords Plus:** ELONGATION-FACTOR-TU; GONOCOCCAL OUTER-MEMBRANE; ESCHERICHIA-COLI; CATHEPSIN-G; GENES; EXPRESSION; SEQUENCE; DNA; MUTATIONS; CLEAVAGE  
**Research Fronts:** 94-4806 003 (GENE ORGANIZATION; LONG-CHAIN FATTY-ACID TRANSPORT; TRANSCRIPTION FACTOR)  
 94-3070 001 (RAT SKELETAL-MUSCLE; DEVELOPMENTAL REGULATION; YEAST SACCHAROMYCES-CEREVISIAE)  
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15/9/29 (Item 3 from file: 34)

DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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04555070 Genuine Article#: TR944 Number of References: 28

**Title: THE HINGE REGION OF ESCHERICHIA-COLI RIBOSOMAL-PROTEIN L7/L12 IS REQUIRED FOR FACTOR-BINDING AND GTP HYDROLYSIS**

Author(s): DEY D; OLEINIKOV AV; TRAUT RR

Corporate Source: UNIV CALIF DAVIS, SCH MED, DEPT BIOL CHEM/DAVIS//CA/95616;  
 UNIV CALIF DAVIS, SCH MED, DEPT BIOL CHEM/DAVIS//CA/95616

Journal: BIOCHIMIE, 1995, V77, N12, P925-930

ISSN: 0300-9084

Language: ENGLISH Document Type: ARTICLE

Geographic Location: USA

Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences

Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY

**Abstract:** A variant form of Escherichia coli ribosomal protein L7/L12 that lacked residues 42 to 52 (L7/L12:Delta 42-52) in the hinge region was shown previously to be completely inactive in supporting polyphenylalanine synthesis although it bound to L7/L12 deficient core particles with the normal stoichiometry of four copies per particle (Oleinikov AV, Perroud B, Wang B, Traut RR (1993) J Biol Chem, 268, 917-922). The result suggested that the hinge confers flexibility that is required for activity because the resulting bent conformation allows the distal C-terminal domain to occupy a location on the body of the

large ribosomal subunit proximal to the base of the L7/L12 stalk where elongation factors bind. Factor binding to the hinge-truncated variant was tested. As an alternative strategy to deleting residues from the hinge, seven amino acid residues within the putative hinge region were replaced by seven consecutive proline residues in an attempt to confer increased rigidity that might reduce or eliminate the bending of the molecule inferred to be functionally important. This variant, L7/L12:(Pro)(7), remained fully active in protein synthesis. Whereas the binding of both factors in ribosomes containing L7/L12:Delta 42-52 was decreased by about 50%, there was no loss of factor binding in ribosomes containing L7/L12:(Pro)(7), as predicted from the retention of protein synthesis activity. The factor:ribosome complexes that contained L7/L12:Delta 42-52 had the same low level of GTP hydrolysis as the core particles completely lacking L7/L12 and EF-G did not support translocation measured by the reaction of phe-tRNA bound in the A site with puromycin. It is concluded that the hinge region is required for the functionally productive binding of elongation factors, and the defect in protein synthesis reported previously is due to this defect. The variant produced by the introduction of the putative rigid Pro(7) sequence retains sufficient flexibility for full activity.

Descriptors--Author Keywords: L7/L12 ; EF-G ; **EF-TU** ; GTP HYDROLYSIS ; HINGE DELETION

Identifiers--KeyWords Plus: NUCLEAR MAGNETIC-RESONANCE; **MONOCLONAL - ANTIBODIES** ; TERMINAL DOMAINS; CROSS-LINKING; L7-L12; SUBUNIT; EPITOPES; LOCALIZATION; LOCATION

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15/9/32 (Item 6 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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03225266 Genuine Article#: NN684 Number of References: 97

Title: PHYLOGENETIC-RELATIONSHIPS OF BACTERIA BASED ON COMPARATIVE  
 SEQUENCE-ANALYSIS OF ELONGATION-FACTOR TU AND ATP-SYNTHASE BETA-SUBUNIT  
 GENES

Author(s): LUDWIG W; NEUMAIER J; KLUGBAUER N; BROCKMANN E; ROLLER C; JILG S  
 ; REETZ K; SCHACHTNER I; LUDVIGSEN A; BACHLEITNER M; FISCHER U;  
 SCHLEIFER KH

Corporate Source: TECH UNIV MUNICH, LEHRSTUHL MIKROBIOL, ARCSSTR 21/D-80290  
 MUNICH//GERMANY//; UNIV OLDENBURG, GEOMIKROBIOL ABT/D-26129

OLDENBURG//GERMANY/

Journal: ANTONIE VAN LEEUWENHOEK INTERNATIONAL JOURNAL OF GENERAL AND  
MOLECULAR MICROBIOLOGY, 1993, V64, N3-4, P285-305

ISSN: 0003-6072

Language: ENGLISH Document Type: ARTICLE

Geographic Location: GERMANY

Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences

Journal Subject Category: MICROBIOLOGY

Abstract: Comparative sequence analyses were performed on 14 genes encoding bacterial elongation factors EF-Tu and 7 genes encoding the beta-subunit of bacterial F1F0 type ATP-synthases. The corresponding predicted amino acid sequences were compared with published primary structures of homologous molecules. Phylogenetic trees were reconstructed from both data sets of aligned protein sequences and from an equivalent selection of 16S rRNA sequences by applying distance matrix and maximum parsimony methods. The EF-Tu data were in very good agreement with the rRNA data, although the resolution within the EF-Tu tree was reduced at certain phylogenetic levels. The resolution power of the ATPase beta-subunit sequence data were more reduced than those of the EF-Tu data. In comparison with the 16S rRNA tree there are minor differences in the order of adjacent branchings within the ATPase beta-subunit tree.

Descriptors--Author Keywords: ATP SYNTHASE BETA-SUBUNIT ; BACTERIA ;  
ELONGATION FACTOR TU ; PHYLOGENY ; SEQUENCE ANALYSIS

Identifiers--KeyWords Plus: PROTON-TRANSLLOCATING ATPASE; DEPENDENT  
RNA-POLYMERASES; NUCLEOTIDE-SEQUENCE; ESCHERICHIA-COLI; **EF-TU**;  
PROPIONIGENIUM-MODESTUM; ENTEROCOCCUS-HIRAE; RIBOSOMAL-RNA; H+-ATPASE;  
MYCOPLASMA-GALLISEPTICUM

Research Fronts: 92-3245 004 (16S RIBOSOMAL-RNA SEQUENCES; PHYLOGENETIC  
CLASSIFICATION; EVOLUTION OF THE HSP70 GENE; SYMBIOTIC BACTERIA)  
92-5433 002 (ATP SYNTHASE OF ESCHERICHIA-COLI; CATALYTIC SITE; SUBUNIT  
B-SPECIFIC **POLYCLONAL ANTIBODIES** )  
92-0229 001 (YEAST ARTIFICIAL CHROMOSOME LIBRARY; ISOLATION OF A  
CANDIDATE GENE; DROSOPHILA GENOME PROJECT)  
92-4812 001 (PUTATIVE ANAEROBIC COPROPORPHYRINOGEN-III OXIDASE IN  
RHODOBACTER-SPHAEROIDES; TRANSCRIPTIONAL REGULATORY ELEMENT; FUNCTIONAL  
EXPRESSION)  
92-7034 001 (MOLECULAR EVOLUTION; BALANCING SELECTION; GENIC  
DIVERGENCE; INTERSPECIFIC GENETIC-VARIABILITY)  
92-7158 001 (LACTIC-ACID BACTERIA; DETECTION OF HISTAMINE FORMING  
MICROORGANISMS; SPECIES-SPECIFIC PROBE FOR AEROMONAS-TROTA SPECIES  
NOVA)

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15/9/35 (Item 9 from file: 34)

DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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01519058 Genuine Article#: HE947 Number of References: 21

**Title: SPECIES DIFFERENTIATION OF MYCOPLASMAS BY EF-TU SPECIFIC MONOCLONAL  
- ANTIBODIES**

Author(s): KAMLA V; HENRICH B; HADDING U

Corporate Source: UNIV DUSSELDORF, INST MED MIKROBIOL & VIROL, MOORENSTR  
5/W-4000 DUSSELDORF 1//GERMANY/

Journal: JOURNAL OF IMMUNOLOGICAL METHODS, 1992, V147, N1 (FEB 14), P73-81

Language: ENGLISH Document Type: ARTICLE

Geographic Location: GERMANY

Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences

Journal Subject Category: IMMUNOLOGY

Abstract: Ten mouse hybridoma cell lines producing IgG monoclonal  
**antibodies** to mycoplasmal elongation factor Tu (EF-Tu) were  
established. These mAbs showed different degrees of cross-reactivity  
between mollicutes and even other bacteria. This finding, indicating  
protein structure diversities of pan bacterial EF-Tu should permit  
species differentiation of mycoplasmas by epitope pattern analysis of a  
single protein. Epitope patterns of 23 mollicute type strains and of  
40 M. hominis isolates were determined by ELISA. All M. hominis  
patterns were found to be closely related whereas intrageneric patterns  
differed in a species specific manner.

Descriptors--Author Keywords: MYCOPLASMA; ELONGATION FACTOR-TU; **MONOCLONAL  
ANTIBODY** ; SPECIES DIFFERENTIATION OF MYCOPLASMAS

Identifiers--KeyWords Plus: POLYMERASE CHAIN-REACTION;

ELONGATION-FACTOR-TU; NUCLEOTIDE-SEQUENCE; GENE; PNEUMONIAE; BINDING

Research Fronts: 90-3110 002 (IDENTIFICATION OF FRAGMENTS;

CORTICOSTEROIDS INCREASE LIPOCORTIN-I; RAS ADENYLATE-CYCLASE PATHWAY;  
HEAT-SHOCK PROTEIN HSP70 FAMILY)

90-3250 001 (16S RIBOSOMAL-RNA; PHYLOGENETIC ANALYSIS; THERMUS SPECIES)

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15/9/39 (Item 13 from file: 34)

DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
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01216903 Genuine Article#: GF348 Number of References: 33

**Title: OVERPRODUCTION OF THE THERMUS-THERMOPHILUS ELONGATION FACTOR-TU IN  
ESCHERICHIA-COLI**

Author(s): AHMADIAN MR; KREUTZER R; SPRINZL M

Corporate Source: UNIV BAYREUTH, BIOCHEM LAB, POSTFACH 101251/D-8580  
BAYREUTH//FED REP GER//; UNIV BAYREUTH, BIOCHEM LAB, POSTFACH  
101251/D-8580 BAYREUTH//FED REP GER//; UNIV BAYREUTH, BAYREUTHER INST  
MAKROMOLEK FORSCH/D-8580 BAYREUTH//FED REP GER/

Journal: BIOCHIMIE, 1991, V73, N7-8, P1037-1043

Language: ENGLISH Document Type: ARTICLE

Geographic Location: FEDERAL REPUBLIC OF GERMANY

Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences

Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY

Abstract: The elongation factor Tu (EF-Tu) encoded by the *tuf1* gene of the extreme thermophilic bacterium *Thermus thermophilus* HB8 was expressed under control of the *tac* promoter from the recombinant plasmid pEFTu-10 in *Escherichia coli*. Thermophilic EF-Tu.GDP, which amounts to as much as 35% of the cellular protein content, was separated from the *E. coli* EF-Tu.GDP by thermal denaturation at 60-degrees-C. The overproduced *E. coli*-born *T. thermophilus* EF-Tu was characterized by: i) recognition through *T. thermophilus* anti-EF-Tu antibodies; ii) analysis of the peptides obtained by cyanogen bromide cleavage; iii) thermostability; iv) guanine nucleotide binding activity in the absence and the presence of elongation factor Ts; and v) ternary complex formation with phenylalanyl-tRNA(Phe) and GTP.

Descriptors--Author Keywords: THERMUS-THERMOPHILUS; SITE-DIRECTED MUTAGENESIS; ELONGATION FACTOR-TU; *ESCHERICHIA-COLI*; GENE EXPRESSION; THERMOPHILIC PROTEINS

Identifiers--KeyWords Plus: POLYPEPTIDE-CHAIN-ELONGATION; BINDING-SITE; TRANSFER-RNA; EXTREME THERMOPHILE; G-PROTEINS; EF-TU; GENE; PURIFICATION; SEQUENCE; CLONING

Research Fronts: 89-1447 002 (DEVELOPMENTALLY REGULATED GENE; CAPPING PROTEIN; CDNA SEQUENCE; GENOME ORGANIZATION)

89-2063 002 (CALCIUM CHANNELS; SMOOTH-MUSCLE CELLS; ISOLATED RAT HYPOTHALAMIC NEURONS)

89-6871 002 (BACTERIAL ELONGATION FACTOR-TU; GTP-BINDING PROTEIN HAVING THE SAME EFFECTOR DOMAIN; ADENYLYL CYCLASE)

89-3034 001 (MICROTUBULE CROSS-LINKING PROTEIN; SMALL SYNAPTIC VESICLES OF RAT-BRAIN; AXOLININ LOCALIZATION)

89-6181 001 (*ESCHERICHIA-COLI* RIBOSOME; THERMUS-THERMOPHILUS ELONGATION FACTOR-TU; 16S RNA IN PROTEIN-SYNTHESIS)

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15/9/40 (Item 14 from file: 34)  
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci  
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00983055 Genuine Article#: FL181 Number of References: 25

Title: **ELONGATION FACTOR-TU IS METHYLATED IN RESPONSE TO NUTRIENT DEPRIVATION IN ESCHERICHIA-COLI**

Author(s): YOUNG CC; BERNLOHR RW

Corporate Source: PENN STATE UNIV,DEPT MOLEC & CELL BIOL/UNIVERSITY  
PK//PA/16802; PENN STATE UNIV,DEPT MOLEC & CELL BIOL/UNIVERSITY  
PK//PA/16802

Journal: JOURNAL OF BACTERIOLOGY, 1991, V173, N10, P3096-3100

Language: ENGLISH Document Type: ARTICLE

Geographic Location: USA

Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences

Journal Subject Category: MICROBIOLOGY

Abstract: It has been shown previously that starvation of a mid-logarithmic-phase culture of *Escherichia coli* B/r for an essential nutrient results in the methylation of a membrane-associated protein (P-43) (C. C. Young and R. W. Bernlohr, J. Bacteriol. 172:5147-5153, 1990). In this communication, the purification of P-43 and sequence analysis of cyanogen bromide-generated peptide fragments identified P-43 as elongation factor Tu (EF-Tu). This was confirmed by the ability of anti-EF-Tu **antibody** to precipitate P-43. We propose that the nutrient-dependent methylation of EF-Tu may be involved in the regulation of growth, possibly as a principal component of an unidentified signal transduction pathway in bacteria.

Identifiers--KeyWords Plus: MEMBRANE-ASSOCIATED PROTEIN; DEPENDENT METHYLATION; **EF-TU**; LOCATION; DOMAIN; SHOCK; HEAT

Research Fronts: 89-0240 001 (RAS P21-LIKE GTP-BINDING PROTEIN; BACTERIAL ELONGATION FACTOR-TU; CELLULAR SIGNAL TRANSDUCTION)

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15/9/49 (Item 2 from file: 144)  
DIALOG(R)File 144:Pascal  
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11456023 PASCAL No.: 94-0290825  
Cloning, sequencing, and expression in *Escherichia coli* of the gene

**encoding a 45-kilodalton protein, elongation factor Tu, from Chlamydia trachomatis serovar F**

YOU-XUN ZHANG; YAN SHI; MIN ZHOU; PETSKE G A

Boston univ. school medicine, Boston City hosp., Maxwell Finland lab.  
infectious diseases, Boston MA 02118, USA

Journal: Journal of bacteriology, 1994, 176 (4) 1184-1187

ISSN: 0021-9193 CODEN: JOBAAY Availability: INIST-2041;  
354000025490960310

No. of Refs.: 22 ref.

Document Type: P (Serial) ; A (Analytic)

Country of Publication: USA

Language: English

The gene encoding a 45-kDa protein (45K) or Chlamydia trachomatis serovar F was cloned, sequenced, and overexpressed in Escherichia coli. Alignment of the deduced peptide sequence with E. coli elongation factor Tu (EF-Tu) demonstrated 69% identity. The 45K was recognized by a Chlamydia-specific monoclonal antibody GP-45 and cross-reacted with a monospecific polyclonal antibody to E. coli EF-Tu. Purified recombinant 45K has the capability to bind GDP, and the binding was enhanced in the presence of E. coli elongation factor Ts (EF-Ts). The GDP binding was specifically inhibited by the monoclonal antibody GP-45

English Descriptors: Chlamydia trachomatis; Elongation factor **EFTu** ; Gene;

Molecular cloning; Structural analysis; Gene expression; Purification

Broad Descriptors: Chlamydiaceae; Chlamydiales; Bacteria; Chlamydiaceae;  
Chlamydiales; Bacterie; Chlamydiaceae; Chlamydiales; Bacteria

French Descriptors: Chlamydia trachomatis; Facteur elongation **EFTu** ; Gene;

Clonage moleculaire; Analyse structurale; Expression genique;

Purification

Classification Codes: 002A05B09

15/9/50 (Item 3 from file: 144)

DIALOG(R) File 144:Pascal

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09164041 PASCAL No.: 90-0332421

**Immunochemical cross-reactivities of protein synthesis elongation factors (EF-Tu and EF-1 alpha proteins) support the phylogenetic coherence of archaeobacteria**

TIBONI O; SANAGELANTONI A M; DI PASQUALE G; CAMMARANO P

Univ. studi Pavia, dip. genetica microbiologia, Pavia 27100, Italy

Journal: Systematic and applied microbiology, 1989, 12 (3) 237-243

ISSN: 0723-2020 CODEN: SAMIDF Availability: INIST-3329C2;  
354000007589050030

No. of Refs.: 28 ref.

Document Type: P (Serial) ; A (Analytic)

Country of Publication: Federal Republic of Germany

Language: English

Elongation factor Tu (EF-tu) proteins have been purified by affinity chromatography on GDP-Sepharose columns, from the eubacterium Thermotoga maritima and from archaeobacteria (Sulfolobus solfataricus, Thermoproteus tenax, Thermococcus celer, Pyrococcus wosei, Archaeoglobus fulgidus, Methanococcus thermolithotrophicus, Thermoplasma acidophilum) representative of all known divisions in the archaeobacterial tree except halophiles.

**Polyclonal antibodies** raised against the purified Tu proteins were challenged with homologous and heterologous factors including eukaryotic EF-1 alpha and cross-reactivities were quantified using SUP 1 SUP 2 SUP 5 I labelled Protein A as the reporter molecule

English Descriptors: Phylogeny; Elongation factor **EFTu** ; Purification;

Immunochemistry; Cross reaction; Antigenic relationship; Immunoblotting

assay; Elongation factor EF1 alpha ; Rat; Eubacteria; Thermotoga maritima  
; Archaeobacteria

Broad Descriptors: Rodentia; Mammalia; Vertebrata; Bacteria; Rodentia;

Mammalia; Vertebrata; Bacterie; Rodentia; Mammalia; Vertebrata; Bacteria

French Descriptors: Phylogenese; Facteur elongation **EFTu** ; Purification; Immunochimie; Reaction croisee; Parente antigenique; Methode immunoblotting; Facteur elongation EF1 alpha ; Rat; Eubacteria; Thermotoga maritima; Archaeobacteria

Classification Codes: 002A07A

15/9/51 (Item 4 from file: 144)  
DIALOG(R) File 144:Pascal  
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08878423 PASCAL No.: 90-0046300

**Unusually strong immunological cross-reaction between elongation factor Tu of Escherichia coli and Bacillus subtilis**

WENZIG P; SCHLEIFER K H

Tech. univ. Muenchen, Lehrstuhl mikrobiologie, Muenchen 8000, Federal Republic of Germany

Journal: Archives of Microbiology, 1989, 152 (3) 258-262

ISSN: 0302-8933 CODEN: AMICW Availability: CNRS-856

No. of Refs.: 34 ref.

Document Type: P (Serial) ; A (Analytic)

Country of Publication: Federal Republic of Germany

Language: English

**Polyclonal antibodies** were prepared against the purified elongation factor Tu of Escherichia coli and Bacillus subtilis. Using the methods of Western blotting and microcomplement fixation the cross-reactivities of EF-Tu of 19 different prokaryotes were determined. An unexpectedly high cross-reactivity was revealed between the EF-Tu of B. subtilis and the **antisera** against the EF-Tu of E. coli

English Descriptors: Elongation factor **EFTu** ; Cross reaction; Immunoblotting assay; Complement fixation test; **Polyclonal immunoglobulin** ; Homology; Aminoacid sequence; Sequence alignment; Phylogeny; Dendrometry; Bacillus subtilis; Escherichia coli

Broad Descriptors: Bacillaceae; Bacillales; Bacteria; Escherichieae; Enterobacteriaceae; Bacillaceae; Bacillales; Bacterie; Escherichieae; Enterobacteriaceae; Bacillaceae; Bacillales; Bacteria; Escherichieae; Enterobacteriaceae

French Descriptors: Facteur elongation **EFTu** ; Reaction croisee; Methode immunoblotting; Test fixation complement; **Immunoglobuline polyclonale** ; Homologie; Sequence aminoacide; Alignement sequence ; Phylogenese; Dendrometrie; Bacillus subtilis; Escherichia coli

Classification Codes: 002A05B02

15/9/52 (Item 5 from file: 144)  
DIALOG(R) File 144:Pascal  
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08023772 PASCAL No.: 88-0023771

**Monoclonal antibodies to epitopes in both C-terminal and N-terminal domains of Escherichia coli ribosomal protein L7/L12 inhibit elongation factor binding but not peptidyl transferase activity**

NAG B; TEWARI D S; TRAUT R R

Univ. California, school medicine, Davis CA 95616, USA

Journal: Biochemistry (Easton), 1987, 26 (2) 461-465

ISSN: 0006-2960 Availability: CNRS-9758

No. of Refs.: 35 ref.

Document Type: P (Serial) ; A (Analytic)

Country of Publication: USA

Language: ENGLISH

English Descriptors: **Monoclonal antibody** ; Antigenic determinant;

Ribosomal protein; Elongation factor; Elongation factor EFG; **Elongation factor EFTu** ; **Translation** ; Escherichia coli; Ribosome; Ternary complex ; C terminal peptide; N terminal peptide; Molecular interaction; Inhibition; GTP  
Broad Descriptors: Escherichieae; Enterobacteriaceae; Bacteria; Escherichieae; Enterobacteriaceae; Bacterie; Escherichieae; Enterobacteriaceae; Bacteria  
French Descriptors: Anticorps **monoclonal** ; Determinant antigenique; Proteine ribosomique; Facteur elongation; Facteur elongation EFG; Facteur elongation **EFTu** ; Traduction; Escherichia coli; Ribosome; Complexe ternaire; Peptide C terminal; Peptide N terminal; Interaction moleculaire ; Inhibition; GTP; Proteine L7; Proteine L12; Peptidyltransferase; TRNA aminoacyl

Classification Codes: 002A04C06

15/9/53 (Item 6 from file: 144)  
DIALOG(R) File 144:Pascal  
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05913012 PASCAL No.: 85-0098066  
**A competitive solid-phase radioimmunoassay for translational factors employing monoclonal antibodies**  
HUTCHINSON J S; FEINBERG B; MOLDAVE K  
Univ. California, coll. medicine, Irvine CA 92717, USA  
Journal: Journal of immunological Methods, 1984, 73 (2) 337-345  
ISSN: 0022-1759 Availability: CNRS-15654  
No. of Refs.: 13 ref.  
Document Type: P (Serial) ; A (Analytic)  
Country of Publication: Netherlands  
Language: English

English Descriptors: **Monoclonal antibody** ; **Translation** ; **Elongation factor** ; Detection; Quantitative analysis; Radioimmunoassay; Solid phase; Affinity chromatography; Protein synthesis; Enzyme; Hybridoma; Proteins

French Descriptors: Anticorps **monoclonal** ; Traduction; Facteur elongation; Detection; Analyse quantitative; Methode radioimmunologique; Phase solide ; Chromatographie affinite; Synthese proteique; Enzyme; Hybridome; Proteine; Facteur traduction; Facteur elongation EF3

Classification Codes: 002A04C06

15/9/67 (Item 2 from file: 434)  
DIALOG(R) File 434:SciSearch(R) Cited Ref Sci  
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09687559 Genuine Article#: AN488 Number of References: 31  
**Title: HOMOLOGIES IN THE STRUCTURES OF G-BINDING PROTEINS - AN ANALYSIS BASED ON ELONGATION-FACTOR EF-TU**  
Author(s): WOOLLEY P; CLARK BFC  
Corporate Source: AARHUS UNIV, DEPT CHEM, DIV BIOSTRUCT CHEM/DK-8000 AARHUS C//DENMARK/  
Journal: BIO-TECHNOLOGY, 1989, V7, N9, P913-920  
Language: ENGLISH Document Type: REVIEW  
Geographic Location: DENMARK  
Subfile: SciSearch; Scisearch; CC LIFE--Current Contents, Life Sciences; CC AGRI--Current Contents, Agriculture, Biology & Environmental Sciences  
Journal Subject Category: BIOTECHNOLOGY & APPLIED MICROBIOLOGY  
Research Fronts: 87-2903 004 (P21 RAS PROTEINS; EXPRESSION OF ONCOGENES; SITE-DIRECTED **MONOCLONAL - ANTIBODY** PROBES)  
87-0968 001 (CONFORMATION OF SHORT LINEAR PEPTIDES; IONIC SOLVATION IN WATER COSOLVENT MIXTURES; PROTEIN FOLDING; REFINED CRYSTAL-STRUCTURE; HYDROPHOBIC INTERACTIONS)  
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15/9/68 (Item 3 from file: 434)

DIALOG(R)File 434:SciSearch(R) Cited Ref Sci

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09545970 Genuine Article#: AA802 Number of References: 68

**Title: THE RHIZOBIUM-MELILOTI HOST RANGE NODQ GENE ENCODES A PROTEIN WHICH SHARES HOMOLOGY WITH TRANSLATION ELONGATION AND INITIATION-FACTORS**

**Author(s): CERVANTES E; SHARMA SB; MAILLET F; VASSE J; TRUCHET G; ROSENBERG C**

Corporate Source: INRA,BIOL MOLEC RELAT PLANTES MICROORGANISMS LAB,CNRS,BP 27/F-31326 CASTANET TOLOSAN//FRANCE/

Journal: MOLECULAR MICROBIOLOGY, 1989, V3, N6, P745-755

Language: ENGLISH Document Type: ARTICLE

Geographic Location: FRANCE

Subfile: SciSearch; Scisearch; CC LIFE--Current Contents, Life Sciences

Journal Subject Category: MICROBIOLOGY

Research Fronts: 87-1403 004 (OPIN GENE; MALIC ENZYME MESSENGER-RNA; CDNA CLONES; STRUCTURAL ORGANIZATION; DISTINCT FORMS)

87-2903 002 (P21 RAS PROTEINS; EXPRESSION OF ONCOGENES; SITE-DIRECTED MONOCLONAL - ANTIBODY PROBES)

87-1387 001 (NODULATION GENES; TRANSCRIPTIONAL ACTIVATION OF THE KLEBSIELLA-PNEUMONIAE NIFH PROMOTER; SYMBIOTIC PLASMID; ESCHERICHIA-COLI GLUTAMINE-SYNTHETASE)

87-2107 001 (MULTIDRUG RESISTANCE; DRUG-SENSITIVE CHINESE-HAMSTER OVARY CELLS; AMPLIFIED MDR1 GENE; P-GLYCOPROTEIN EXPRESSION)

87-3538 001 (ESCHERICHIA-COLI RNA-POLYMERASE; PROMOTER RECOGNITION; STRUCTURAL GENE; TRANSCRIPTION INITIATION; NUCLEOTIDE-SEQUENCE HOMOLOGIES; TRANSLATIONAL REQUIREMENT)

87-7383 001 (ZEA CHLOROPLAST GENOME; 5S RIBOSOMAL-RNA GENE; SEQUENCE OF THE MAIZE PLASTID ENCODED RPL 22 LOCUS)

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05nov03 14:26:40 User228206 Session D2080.5  
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### Status: Signed Off. (1 minutes)

File 155: Please see HELP NEWS 155 for details about the 2003 reload.

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Set  Items  Description
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?e ef-tu
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Ref	Items	RT	Index-term
E1	1		EF-C
E2	2	1	EF-G
E3	5		*EF-TU
E4	1	1	EF-1
E5	12		EF-1 ALPHA
E6	1		EF-1 ALPHA O
E7	1		EF-1 BETA
E8	1	1	EF-2
E9	1		EF-3
E10	4		EF-3A PROTEIN
E11	1		EF-3B PROTEIN
E12	791		EFA

Enter P or PAGE for more

?s e3

S1 5 'EF-TU'

?e translation elongation factor

Ref	Items	RT	Index-term
E1	188		TRANSLATION //POLARITY OF (POLARITY OF TRANSLATION)
E2	3		TRANSLATION ANTI-INHIBITOR
E3	0		*TRANSLATION ELONGATION FACTOR
E4	0	1	TRANSLATION INITIATION FACTORS, EUKARYOTIC
E5	0	1	TRANSLATION INITIATION FACTORS, PROKARYOTIC
E6	28460	13	TRANSLATION, GENETIC
E7	3889		TRANSLATION, GENETIC --DRUG EFFECTS --DE
E8	782		TRANSLATION, GENETIC --GENETICS --GE
E9	51		TRANSLATION, GENETIC --IMMUNOLOGY --IM
E10	490		TRANSLATION, GENETIC --PHYSIOLOGY --PH
E11	79		TRANSLATION, GENETIC --RADIATION EFFECTS --RE
E12	1		TRANSLATIONA

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?e e5

Ref	Items	Type	RT	Index-term
R1	0		1	*TRANSLATION INITIATION FACTORS, PROKARYOTIC
R2	2	X	7	PROKARYOTIC INITIATION FACTORS

?s r2

S2 2 'PROKARYOTIC INITIATION FACTORS'

?e r2

Ref	Items	Type	RT	Index-term
R1	2		7	*PROKARYOTIC INITIATION FACTORS
R2	2	X		DC=D12.776.835.725.934. (PROKARYOTIC INITIATION FACTORS)
R3	0	X	1	PEPTIDE INITIATION FACTORS, PROKARYOTIC
R4	0	X	1	TRANSLATION INITIATION FACTORS, PROKARYOTIC
R5	2819	B	18	PEPTIDE INITIATION FACTORS
R6	1	N	3	PROKARYOTIC INITIATION FACTOR-1
R7	90	N	3	PROKARYOTIC INITIATION FACTOR-2
R8	125	N	3	PROKARYOTIC INITIATION FACTOR-3

?s r1-r8

2 PROKARYOTIC INITIATION FACTORS  
2 DC=D12.776.835.725.934. (PROKARYOTIC INITIATION FACTORS)  
0 PEPTIDE INITIATION FACTORS, PROKARYOTIC  
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2819 PEPTIDE INITIATION FACTORS  
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90 PROKARYOTIC INITIATION FACTOR-2  
125 PROKARYOTIC INITIATION FACTOR-3  
S3 2837 R1-R8

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S1	5	'EF-TU'
S2	2	'PROKARYOTIC INITIATION FACTORS'
S3	2837	R1-R8
?s translation? (2n) elongat? (2n) factor?		
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	2023420	FACTOR?
S4	407	TRANSLATION? (2N) ELONGAT? (2N) FACTOR?

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Ref	Items	Index-term
E1	1	EFTSA
E2	1	EFTT
E3	25	*EFTU
E4	1	EFTUA
E5	7	EFT1
E6	8	EFT2
E7	1	EFT2P
E8	2	EFT4
E9	22	EFU
E10	1	EFUAMIDE
E11	3	EFUC
E12	4	EFUCATTLE

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?s e3 or e4

	25	EFTU
	1	EFTUA
S5	26	'EFTU' OR 'EFTUA'

?ds

Set	Items	Description
S1	5	'EF-TU'
S2	2	'PROKARYOTIC INITIATION FACTORS'
S3	2837	R1-R8
S4	407	TRANSLATION? (2N) ELONGAT? (2N) FACTOR?
S5	26	'EFTU' OR 'EFTUA'
?s (s1 or s2 or s3 or s4 or s5) and ((amino or n) (3n) terminal?)		
	5	S1
	2	S2
	2837	S3
	407	S4
	26	S5
	526811	AMINO
	624930	N
	233559	TERMINAL?
	77226	(AMINO OR N) (3N) TERMINAL?
S6	176	(S1 OR S2 OR S3 OR S4 OR S5) AND ((AMINO OR N) (3N) TERMINAL?)

?s s6 and (antibod? or immune? or immunoglob? or antiser? or igg or iga or igm or monoclonal? or polyclonal? or mab or moab or antiser?)

	176	S6
	631146	ANTIBOD?
	240770	IMMUNE?
	207169	IMMUNOGLOB?
	54125	ANTISER?
	77116	IGG
	29942	IGA
	39798	IGM
	170885	MONOCLONAL?
	35046	POLYCLONAL?
	24827	MAB
	3393	MOAB
	54125	ANTISER?
S7	17	S6 AND (ANTIBOD? OR IMMUNE? OR IMMUNOGLOB? OR ANTISER? OR IGG OR IGA OR IGM OR MONOCLONAL? OR POLYCLONAL? OR MAB OR

· MOAB OR ANTISER?)

0383819 96189112 PMID: 8628297

**SUI1/p16 is required for the activity of eukaryotic translation initiation factor 3 in *Saccharomyces cerevisiae*.**

Naranda T; MacMillan S E; Donahue T F; Hershey J W  
Department of Biological Chemistry, School of Medicine, University of California, Davis, 95616, USA.

Molecular and cellular biology (UNITED STATES) May 1996, 16 (5)  
p2307-13, ISSN 0270-7306 Journal Code: 8109087

Contract/Grant No.: GM22135; GM; NIGMS; GM32263; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A genetic reversion analysis at the HIS4 locus in *Saccharomyces cerevisiae* has identified SUI1 as a component of the translation initiation complex which plays an important role in ribosomal recognition of the initiator codon. SUI1 is an essential protein of 12.3 kDa that is required in vivo for the initiation of protein synthesis. Here we present evidence that SUI1 is identical to the smallest subunit, p16, of eukaryotic translation initiation factor 3 (eIF-3) in *S. cerevisiae*. SUI1 and eIF3-p16 comigrate upon sodium dodecyl sulfate-polyacrylamide gel electrophoresis and cross-react with anti-SUI1 and anti-eIF3 **antisera**. Anti-SUI1 **antisera** immunoprecipitate all of the subunits of eIF3, whereas **antisera** against the eIF3 complex and the individual PRT1 and GCD10 subunits of eIF3 immunoprecipitate SUI1. Finally, the N - terminal amino acid sequence of a truncated form of eIF3-p16 matches the sequence of SUI1. eIF3 isolated from a *suil(ts)* strain at 37 degrees C lacks SUI1 and fails to exhibit eIF3 activity in the in vitro assay for methionyl-puromycin synthesis. A free form of SUI1 separate from the eIF3 complex is found in *S. cerevisiae* but lacks activity in the in vitro assay. The results, together with prior genetic experiments, indicate that SUI1 is essential for eIF3 activity and functions as part of eIF3 and in concert with eIF2 to promote eIF2-GTP-Met-tRNAi ternary complex recognition of the initiator codon.

Tags: Comparative Study; Human; Support, U.S. Gov't, P.H.S.

Descriptors: Fungal Proteins--genetics--GE; \*Fungal Proteins--metabolism--ME; \* **Peptide Initiation Factors** --metabolism--ME; \**Saccharomyces cerevisiae*--metabolism--ME; \*Transcription Factors--genetics--GE; Amino Acid Sequence; Electrophoresis, Polyacrylamide Gel; Eukaryotic Initiation Factor-3; Fungal Proteins--biosynthesis--BI; Fungal Proteins--chemistry--CH; Fungal Proteins--isolation and purification--IP; Genes, Fungal; Hela Cells; Kinetics; Macromolecular Systems; Molecular Sequence Data; **Peptide Initiation Factors** --chemistry--CH; **Peptide Initiation Factors** --isolation and purification--IP; Ribosomes--metabolism--ME; *Saccharomyces cerevisiae*--genetics--GE; Sequence Homology, Amino Acid; Transcription Factors--biosynthesis--BI

CAS Registry No.: 0 (Eukaryotic Initiation Factor-3); 0 (Fungal Proteins); 0 (His4 protein); 0. (Macromolecular Systems); 0 (Peptide Initiation Factors); 0 (Transcription Factors); 144814-03-9 (*suil* protein)

Record Date Created: 19960621

Record Date Completed: 19960621

7/9/7

DIALOG(R) File 155:MEDLINE(R)

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09431437 21199402 PMID: 11302750

**Rpg1p/Tif32p, a subunit of translation initiation factor 3, interacts with actin-associated protein Sla2p.**

Palecek J; Hasek J; Ruis H

Vienna Biocenter, Institute of Biochemistry and Molecular Cell Biology, University of Vienna, Austria.

Biochemical and biophysical research communications (United States) Apr 20 2001, 282 (5) p1244-50, ISSN 0006-291X Journal Code: 0372516

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The yeast two-hybrid system was used to screen for proteins that interact in vivo with *Saccharomyces cerevisiae* Rpg1p/Tif32p, the large subunit of the translation initiation factor 3 core complex (eIF3). Eight positive clones encoding portions of the SLA2/END4/MOP2 gene were isolated. They overlapped in the region of amino acids 318-550. Subsequent deletion analysis of Sla2p showed that amino acids 318-373 were essential for the two-hybrid protein-protein interaction. The N - terminal part of Rpg1p (aa 1-615) was essential and sufficient for the Rpg1p-Sla2p interaction. A coimmunoprecipitation assay provided additional evidence for the physical interaction of Rpg1p/Tif32p with Sla2p in vivo. Using immunofluorescence microscopy, Rpg1p and Sla2p proteins were colocalized at the patch associated with the tip of emerging bud. Considering the essential role of Rpg1p as the large subunit of the eIF3 core complex and the association of Sla2p with the actin cytoskeleton, a putative role of the Rpg1p-Sla2p interaction in localized translation is discussed. Copyright 2001 Academic Press.

Tags: Support, Non-U.S. Gov't

Descriptors: Actins--metabolism--ME; \*Carrier Proteins--metabolism--ME; \*Cell Cycle Proteins--metabolism--ME; \*Fungal Proteins--metabolism--ME; \*Peptide Initiation Factors --metabolism--ME; Carrier Proteins--genetics--GE; Cell Cycle Proteins--genetics--GE; Cytoskeleton--metabolism--ME; Eukaryotic Initiation Factor-3; Fluorescent Antibody Technique; Fungal Proteins--genetics--GE; Genes, Reporter; Mutagenesis, Site-Directed; Precipitin Tests; Protein Binding--physiology--PH; Protein Structure, Tertiary--physiology--PH; Protein Subunits; *Saccharomyces cerevisiae*; Two-Hybrid System Techniques

CAS Registry No.: 0 (Actins); 0 (Carrier Proteins); 0 (Cell Cycle Proteins); 0 (Eukaryotic Initiation Factor-3); 0 (Fungal Proteins); 0 (Peptide Initiation Factors); 0 (Protein Subunits); 0 (RPG1 protein); 0 (SLA2 protein)

Record Date Created: 20010416

Record Date Completed: 20010517

7/9/8

DIALOG(R) File 155:MEDLINE(R)

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09350867 21112174 PMID: 11161987

**Cross-reaction of lupus anti-dsDNA antibodies with protein translation factor EF-2.**

Alberdi F; Dadone J; Ryazanov A; Isenberg D A; Ravirajan C; Reichlin M  
Arthritis and Immunology Program, University of Oklahoma Health Sciences Center, Oklahoma City, Oklahoma 73104, USA.

Clinical immunology (Orlando, Fla.) (United States) Feb 2001, 98 (2)  
p293-300, ISSN 1521-6616 Journal Code: 100883537

Contract/Grant No.: R01 AR43975; AR; NIAMS

Erratum in Clin Immunol 2001 Jul;100(1) 127

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

This report elucidates a new cross-reactive intracellular target of anti-dsDNA antibodies. Previous experiments have demonstrated that some anti-dsDNA antibodies penetrate cells grown in tissue culture and all inhibit in vitro translation. Data implicate a cross-reactive antigen directly involved in protein synthesis: elongation factor-2 (EF-2). EF-2 was identified by N - terminal sequencing of a band identified with an antibody to the ribosomal protein S1 from *Leuconostoc lactis* in Western blot assay. Anti-DNA antibodies bind directly to purified EF-2 from bovine liver in dot blot assays. Anti-dsDNA antibodies were shown to inhibit in vitro translation. This inhibiting effect of anti-dsDNA antibodies was partially restored by EF-2 and abrogated by dsDNA, suggesting this cross-reactive specificity. These data demonstrate a cross-reaction between anti-dsDNA antibodies and EF-2 which may lead to

cellular dysfunction, as evidenced by inhibition of protein synthesis, and provide a direct pathogenic role for cell penetrating anti-dsDNA **antibodies** . Copyright 2000 Academic Press.

Tags: Animal; Comparative Study; Human; Support, U.S. Gov't, P.H.S.

Descriptors: **Antibodies** , Antinuclear--immunology--IM; \*Autoantigens --immunology--IM; \*Autoimmune Diseases--immunology--IM; \*DNA--immunology --IM; \* **Immunoglobulin G**--immunology--IM; \*Lupus Erythematosus, Systemic --immunology--IM; \***Peptide Elongation Factor 2**--immunology--IM; \* **Translation** , Genetic--immunology--IM; **Antibodies** , Antinuclear --pharmacology--PD; **Antibodies** , **Monoclonal** --immunology--IM; **Antibodies** , **Monoclonal** --pharmacology--PD; **Antibody Specificity**; Cattle; Cross Reactions; Hela Cells; Liver--chemistry--CH; Peptide Elongation Factor 2--isolation and purification--IP; Rabbits; Ribosomal Proteins--immunology--IM; Translation, Genetic--drug effects--DE

CAS Registry No.: 0 (Antibodies, Antinuclear); 0 (Antibodies, Monoclonal); 0 (Autoantigens); 0 (Immunoglobulin G); 0 (Peptide Elongation Factor 2); 0 (Ribosomal Proteins); 0 (ribosomal protein S1); 9007-49-2 (DNA)

Record Date Created: 20010222

Record Date Completed: 20010329

7/9/9

DIALOG(R) File 155:MEDLINE(R)

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09252281 20566685 PMID: 11114918

**Initiation factor 2 of Myxococcus xanthus, a large version of prokaryotic translation initiation factor 2.**

Tiennault-Desbordes E; Cenatiempo Y; Laalami S

Institut de Biologie Moleculaire et d'Ingenierie Genetique, ESA CNRS 6031, Universite de Poitiers, 86022 Poitiers Cedex, France.

Journal of bacteriology (UNITED STATES) Jan 2001, 183 (1) p207-13, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

We have isolated the structural gene for translation initiation factor IF2 (infB) from the myxobacterium *Myxococcus xanthus*. The gene (3.22 kb) encodes a 1,070-residue protein showing extensive homology within its G domain and C terminus to the equivalent regions of IF2 from *Escherichia coli*. The protein cross-reacts with **antibodies** raised against *E. coli* IF2 and was able to complement an *E. coli* infB mutant. The *M. xanthus* protein is the largest IF2 known to date. This is essentially due to a longer **N-terminal** region made up of two characteristic domains. The first comprises a 188-amino-acid sequence consisting essentially of alanine, proline, valine, and glutamic acid residues, similar to the APE domain observed in *Stigmatella aurantiaca* IF2. The second is unique to *M. xanthus* IF2, is located between the APE sequence and the GTP binding domain, and consists exclusively of glycine, proline, and arginine residues.

Tags: Support, Non-U.S. Gov't

Descriptors: *Myxococcus xanthus*--genetics--GE; \* **Peptide Initiation Factors** --chemistry--CH; \* **Peptide Initiation Factors** --genetics--GE; \* **Peptide Initiation Factors** --metabolism--ME; Amino Acid Sequence; Cloning, Molecular; *Escherichia coli*--genetics--GE; *Escherichia coli*--metabolism --ME; Genes, Structural, Bacterial; Genetic Complementation Test; Molecular Sequence Data; Mutation; *Myxococcus xanthus*--metabolism--ME; Plasmids --genetics--GE; **Prokaryotic Initiation Factor-2** ; Protein Structure, Tertiary; Sequence Alignment; Sequence Analysis, DNA; Transformation, Bacterial

Molecular Sequence Databank No.: GENBANK/AF261103

CAS Registry No.: 0 (Peptide Initiation Factors); 0 (Plasmids); 0 (Prokaryotic Initiation Factor-2)

Record Date Created: 20001229

Record Date Completed: 20010118



7/9/10

DIALOG(R) File 155:MEDLINE(R)

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09217476 20527427 PMID: 11077990

**Antibodies against mycobacterial antigens in the synovial fluid of patients with temporomandibular disorders.**

Adachi N; Matsumoto S; Tokuhisa M; Kobayashi K; Yamada T

Department of Orthodontics, Nagasaki University School of Dentistry, Sakamoto, Japan.

Journal of dental research (UNITED STATES) Oct 2000, 79 (10) p1752-7

, ISSN 0022-0345 Journal Code: 0354343

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: DENTAL; INDEX MEDICUS

In the absence of active pulmonary disease, mycobacterial infection frequently causes arthritis and can be considered to initiate autoimmune diseases such as rheumatoid arthritis. Temporomandibular disorder (TMD) is a disease in which pain and impaired mandibular movement appear to arise directly from degenerative or inflammatory changes within the temporomandibular joint, but its precise pathogeny has not been elucidated. Here we examined whether mycobacterial infection is related to the pathology of TMD. The **antibody** levels against mycobacterial antigen in the synovial fluid (SF) of patients with TMD were assessed by enzyme-linked immunosorbent assay (ELISA). Six of 17 TMD patients (35%) were found to possess mycobacterial antigen-specific **immunoglobulin** (Ig) G but not **IgM**, while the six healthy volunteers possessed neither. Western-blot analysis was used to isolate the reacted antigen, and the **IgG** reacted strongly to 44-kDa antigen. The first 14 N-terminal amino acid sequences were determined, and computer analysis revealed that it was homologous to **translational elongation factor Tu** (EF-Tu) of Mycobacterium tuberculosis, which was a major target antigen for these **antibodies**. The 44-kDa protein of Mycobacterium bovis BCG (BCG) was identical with the EF-Tu of M. tuberculosis. We cloned the gene encoding the EF-Tu of BCG by using the synthesized oligonucleotide primers by means of polymerase chain-reaction. The gene was expressed in Escherichia coli. The protein was purified, and the **antibody** levels against this recombinant protein in the SF of TMD patients were assessed by ELISA. Our findings suggest that some cases of TMD are concerned with the synovial **IgG** against the EF-Tu of M. tuberculosis, and that the existence of the **antibody** is a clinical indication of TMD.

Tags: Female; Human; Male; Support, Non-U.S. Gov't

Descriptors: \*Mycobacterium--pathogenicity--PY; \*Temporomandibular Joint Disorders--immunology--IM; \*Temporomandibular Joint Disorders--microbiology--MI; Adolescent; Adult; Aged; Amino Acid Sequence; **Antibodies**, Bacterial--analysis--AN; Antigens, Bacterial--immunology--IM; Base Sequence; Blotting, Western; Case-Control Studies; Cloning, Molecular; Electrophoresis, Polyacrylamide Gel; Enzyme-Linked Immunosorbent Assay; **Immunoglobulin G**--analysis--AN; Middle Age; Mycobacterium--immunology--IM; Mycobacterium bovis--immunology--IM; Mycobacterium bovis--pathogenicity--PY; Mycobacterium tuberculosis--immunology--IM; Mycobacterium tuberculosis--pathogenicity--PY; Peptide Elongation Factor Tu--immunology--IM; Recombinant Proteins--immunology--IM; Statistics, Nonparametric; Synovial Fluid--immunology--IM

CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Antigens, Bacterial); 0 (Immunoglobulin G); 0 (Recombinant Proteins)

Enzyme No.: EC 3.6.1.- (Peptide Elongation Factor Tu)

Record Date Created: 20001204

Record Date Completed: 20001204

7/9/11

DIALOG(R) File 155:MEDLINE(R)

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08091094 94156850 PMID: 8113185

**The Myxococcus xanthus dsr gene product performs functions of translation**

**initiation factor IF3 in vivo.**

Kalman L V; Cheng Y L; Kaiser D  
Department of Biochemistry, Stanford University, School of Medicine,  
California 94305.

Journal of bacteriology (UNITED STATES) Mar 1994, 176 (5) p1434-42,  
ISSN 0021-9193 Journal Code: 2985120R  
Contract/Grant No.: GM23441; GM; NIGMS  
Document type: Journal Article  
Languages: ENGLISH  
Main Citation Owner: NLM  
Record type: Completed  
Subfile: INDEX MEDICUS

The amino acid sequence of the Dsg protein is 50% identical to that of translation initiation factor IF3 of *Escherichia coli*, the product of its *infC* gene. Anti-*E. coli* IF3 **antibodies** cross-react with the Dsg protein. Tn5 insertion mutations in *dsg* are lethal. When ample nutrients are available, however, certain *dsg* point mutant strains grow at the same rate as wild-type cells. Under the starvation conditions that induce fruiting body development, these *dsg* mutants begin to aggregate but fail to develop further. The level of Dsg antigen, as a fraction of total cell protein, does not change detectably during growth and development, as expected for a factor essential for protein synthesis. The amount of IF3 protein in *E. coli* is known to be autoregulated at the translational level. This autoregulation is lost in an *E. coli* *infC362* missense mutant. The *dsg+* gene from *Myxococcus xanthus* restores normal autoregulation to the *infC362* mutant strain. Dsg is distinguished from IF3 of *E. coli*, other enteric bacteria, and *Bacillus stearothermophilus* by having a C- **terminal** tail of 66 **amino** acids. Partial and complete deletion of this tail showed that it is needed for certain vegetative and developmental functions but not for viability.

Tags: Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: Bacterial Proteins--metabolism--ME; \**Myxococcus xanthus* --genetics--GE; \**Myxococcus xanthus*--metabolism--ME; \* **Peptide Initiation Factors** --metabolism--ME; \*Trans-Activators--metabolism--ME; Amino Acid Sequence; Bacterial Proteins--biosynthesis--BI; Bacterial Proteins --genetics--GE; Base Sequence; Chromosomes, Bacterial; *Escherichia coli* --metabolism--ME; Genes, Bacterial; Molecular Sequence Data; Molecular Weight; Mutagenesis, Site-Directed; Oligodeoxyribonucleotides; Plasmids; **Prokaryotic Initiation Factor-3** ; Recombinant Proteins--biosynthesis--BI; Recombinant Proteins--metabolism--ME; Recombination, Genetic; Restriction Mapping; Trans-Activators--biosynthesis--BI; Trans-Activators--genetics --GE; Translation, Genetic

CAS Registry No.: 0 (Bacterial Proteins); 0 (Oligodeoxyribonucleotides); 0 (Peptide Initiation Factors); 0 (Plasmids); 0 (Prokaryotic Initiation Factor-3); 0 (Recombinant Proteins); 0 (Trans-Activators); 0 (*dsg* protein)

Gene Symbol: *dsg*; *infC*

Record Date Created: 19940330

Record Date Completed: 19940330

7/9/12

DIALOG(R) File 155:MEDLINE(R)

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07654136 93109337 PMID: 8417348

**GCD11, a negative regulator of GCN4 expression, encodes the gamma subunit of eIF-2 in *Saccharomyces cerevisiae*.**

Hannig E M; Cigan A M; Freeman B A; Kinzy T G

Molecular and Cell Biology Program, University of Texas, Dallas 830688.

Molecular and cellular biology (UNITED STATES) Jan 1993, 13 (1)  
p506-20, ISSN 0270-7306 Journal Code: 8109087

Contract/Grant No.: GM26796; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The eukaryotic translation initiation factor eIF-2 plays a critical role in regulating the expression of the yeast transcriptional activator GCN4. Mutations in genes encoding the alpha and beta subunits of eIF-2 alter translational efficiency at the GCN4 AUG codon and constitutively elevate GCN4 translation. Mutations in the yeast GCD11 gene have been shown to confer a similar phenotype. The nucleotide sequence of the cloned GCD11 gene predicts a 527-amino-acid polypeptide that is similar to the prokaryotic translation elongation factor EF-Tu. Relative to EF-Tu, the deduced GCD11 amino acid sequence contains a 90- amino -acid N - terminal extension and an internal cysteine-rich sequence that contains a potential metal-binding finger motif. We have identified the GCD11 gene product as the gamma subunit of eIF-2 by the following criteria: (i) sequence identities with mammalian eIF-2 gamma peptides; (ii) increased eIF-2 activity in extracts prepared from cells cooverexpressing GCD11, eIF-2 alpha, and eIF-2 beta; and (iii) cross-reactivity of **antibodies** directed against the GCD11 protein with the 58-kDa polypeptide present in purified yeast eIF-2. The predicted GCD11 polypeptide contains all of the consensus elements known to be required for guanine nucleotide binding, suggesting that, in *Saccharomyces cerevisiae*, the gamma subunit of eIF-2 is responsible for GDP-GTP binding.

Tags: Animal; Comparative Study; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: \*Eukaryotic Initiation Factor-2--genetics--GE; \*Fungal Proteins--genetics--GE; \*GTP-Binding Proteins--genetics--GE; \*Genes, Structural, Fungal; \*Protein Kinases--genetics--GE; \**Saccharomyces cerevisiae*--genetics--GE; \*Transcription Factors--genetics--GE; Amino Acid Sequence; Base Sequence; Cloning, Molecular; Cross Reactions; DNA, Fungal --genetics--GE; Eukaryotic Initiation Factor-2--chemistry--CH; Eukaryotic Initiation Factor-2--immunology--IM; GTP-Binding Proteins--metabolism--ME; Gene Expression; Gene Expression Regulation, Fungal; Macromolecular Systems ; Molecular Sequence Data; Oligodeoxyribonucleotides--chemistry--CH; Peptide Elongation Factor Tu--genetics--GE; RNA, Fungal--genetics--GE; RNA, Messenger--genetics--GE; Rabbits; Restriction Mapping; Sequence Alignment; Swine

Molecular Sequence Databank No.: GENBANK/L04268

CAS Registry No.: 0 (DNA, Fungal); 0 (Eukaryotic Initiation Factor-2); 0 (Fungal Proteins); 0 (GCN proteins); 0 (Macromolecular Systems); 0 (Oligodeoxyribonucleotides); 0 (RNA, Fungal); 0 (RNA, Messenger); 0 (Transcription Factors)

Enzyme No.: EC 2.7.1.37 (Protein Kinases); EC 3.6.1.- (GTP-Binding Proteins); EC 3.6.1.- (Peptide Elongation Factor Tu)

Gene Symbol: **EF-Tu** ; GCD11; GCN4; GST1

Record Date Created: 19930127

Record Date Completed: 19930127

7/9/13

DIALOG(R) File 155:MEDLINE(R)

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07595136 93050179 PMID: 1426242

**Tandem translation of *Bacillus subtilis* initiation factor IF2 in *E. coli*. Over-expression of infBB.su in *E. coli* and purification of alpha- and beta-forms of IF2B.su.**

Hubert M; Nyengaard N R; Shazand K; Mortensen K K; Lassen S F; Grunberg-Manago M; Sperling-Petersen H U

Department of Chemistry, Aarhus University, Denmark.

FEBS letters (NETHERLANDS) Nov 9 1992, 312 (2-3) p132-8, ISSN 0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The protein synthesis initiation factor, IF2, in *Bacillus subtilis* has previously been characterized as being present in two forms, alpha and beta, of molecular mass 79 and 68 kDa, respectively, on the basis of their cross-reaction with anti-*E. coli* IF2 **antibodies** and by the DNA sequence of the gene for IF2, infBB.su. In this work we have cloned infBB.su in *E.*

03850476 EMBASE No: 1989019431

**Production and characterisation of monoclonal antibodies specific for staphylococcal enterotoxin B**

Lin Y.-S. ; Lagen M.T. ; Newcomb J.R. ; Rogers T.J.

Department of Microbiology and Immunology, Temple University School of Medicine, Philadelphia, PA 19140 United States

Journal of Medical Microbiology ( J. MED. MICROBIOL. ) (United Kingdom) 1988, 27/4 (263-270)

CODEN: JMMIA ISSN: 0022-2615

DOCUMENT TYPE: Journal

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

We have generated **monoclonal antibodies** (MABs) to staphylococcal enterotoxin B (SEB) in BALB/c mice. Five out of 20 clones which produce anti-SEB MABs have been characterised. Among them, three produce IgGinf 1/kappa, one produces IgM/lambda, and one apparently produces both IgGinf 1/lambda and IgM/lambda MABs. The anti-SEB titres of ascites fluids range from 3200 to >819200 by ELISA. All of the MABs analysed thus far neutralise the mitogenic response of BALB/c splenocytes to a suboptimal dose of SEB. Also, the induction of suppressor cells by SEB in vitro is reversed by pre-incubating SEB with these MABs. **Limited digestion** with chymotrypsin, trypsin or Staphylococcus aureus V8 protease yields peptide fragments which have been tested by Western-blot analysis. MABs 1FD7 and 2GD9 are specific for the carboxy-terminal end of SEB, and have a similar, but not identical, binding epitope. MABs 2DA3 and 2HA10 bind to intact SEB but not to cleaved products, and are probably specific for antigenic determinants altered by the cleavage or by the denaturing conditions of the electrophoresis, or by both.

**DRUG DESCRIPTORS:**

\*enterotoxin; \* **monoclonal antibody**

**MEDICAL DESCRIPTORS:**

\* **antibody** production; \*staphylococcus

hybridoma; immunoblotting; mitogenesis; mouse; radioimmunoassay; nonhuman; animal experiment; priority journal

**MEDICAL TERMS (UNCONTROLLED):** protein digestion

**SECTION HEADINGS:**

004 Microbiology: Bacteriology, Mycology, Parasitology and Virology

026 Immunology, Serology and Transplantation

[Anti-~~Hp~~ antibody may vary with strain used as antigen possibly due to serological diversity]

Mizuta T ; Inoue H; Hayashi T; Shimoyama T

Internal Medicine IV of Hyogo Medical University.

Nippon rinsho (JAPAN) Dec 1993 , 51 (12) p3087-93, ISSN 0047-1852

Journal Code: KIM

Languages: JAPANESE Summary Languages: ENGLISH

Document type: JOURNAL ARTICLE English Abstract

JOURNAL ANNOUNCEMENT: 9404

Subfile: INDEX MEDICUS

Western blotting and ELISA techniques have been used to investigate antigen specificity of systemic responses. Immunoblotting studies demonstrate several major protein antigens that are detected most sera. H. pylori immunoblotting studies using rabbit hyperimmune sera identify several distinct strains. Seven monoclonal antibodies which are prepared in our laboratory recognize 33-35 kDa and 66 kDa of H. pylori. ELISA studies using the monoclonal antibody reveals considerable antigenic diversity among H. pylori strains. Serotyping of clinically isolated H. pylori seems to be useful in clarifying the etiological roles of this bacteria. In spite of studies by several investigators, serotyping of H. pylori has not been established yet. Our studies suggest that H. pylori need to be further subdivided serologically.

Tags: Animal; Human

Descriptors: Antibodies, Bacterial--Isolation and Purification--IP; \*

**Helicobacter** pylori--Immunology--IM; Antibody Diversity; Epitopes; Rabbits; Species Specificity

CAS Registry No.: 0 (Antibodies, Bacterial); 0 (Epitopes)

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**STIC-ILL**

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**Subject:** 09/488,737

*MIC*  
*QB46.J87*

Identification of *Helicobacter pylori* by immunological dot blot method based on reaction of a species-specific monoclonal antibody with a surface-exposed protein.

Bolin I; Lonroth H; Svennerholm AM  
Department of Medical Microbiology and Immunology, Goteborg University, Sweden.

**Journal of clinical microbiology (UNITED STATES) Feb 1995, 33 (2)**  
**p381-4**, ISSN 0095-1137 Journal Code: HSH

Languages: ENGLISH

Document type: JOURNAL ARTICLE

JOURNAL ANNOUNCEMENT: 9507

Subfile: INDEX MEDICUS

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